

GenCore version 5.1.4_p5_4578
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4 nucleic - nucleic search, using sw model
 run on: March 13, 2003, 13:29:58 ; search time 2 Seconds
 (without alignments)
 3.694 Million cell updates/sec

title: us-09-837-602-1
 effect score: 4403
 sequence: 1 ttccggcacggggcgccgttgc.....accgcgtggagctccaggct 4403

scoring table: IDENTITY_NUC
 GapOp 10.0 , Gapext. 0.5

searched: 2 seqs, 839 residues

total number of hits satisfying chosen parameters: 4

minimum DB seq length: 0
 maximum DB seq length: 200000000

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 2 summaries

database :
 1: /home/sdavid/sdavid-tmp/mar03/yu602/aa577530.gb_estl.*
 2: /home/sdavid/sdavid-tmp/mar03/yu602/aa535711.gb_estl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Query Score	Match Length	DB ID	Description
c 1	429.4	9.8	AA577530 1	EST 03-SEB mRNA clone IMAGE:1083831
c 2	408	9.3	AA535711 2	ACCESSION:AA535711

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	COMMENT
AA577530	AA577530	AA577530_1	AA577530	AA577530_1	EST	human.	Homo sapiens	Unpublished (1997)
	AA577530_1	AA577530_1	AA577530_1	AA577530_1			Eukaryota; Chordata; Craniata; Vertebrata; Buteleostei.	Contact: Robert Straussberg, Ph.D.
							Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Email: cgaps-f@mail.nih.gov
							1 (bases 1 to 431)	Procurement: L. Jeffrey Medeiros, M.D., Michael R.
							NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	Emmert-Buck, M.D., Ph.D.
							National Cancer Institute, Cancer Genome Anatomy Project (CGA)	CGNA Library Arrayed by: Greg Lennon, Ph.D.
							Tumor Gene Index	DNA Sequencing by: Washington University Genome Sequencing C

JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbsr@mail.nih.gov
 Ph.D. Tissue Procurement: M. Bento Soares, Ph.D.
 CDNA Library Preparation: Michael R. Emmert-Buck, M.D.
 DNA Sequencing by: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
 Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbfp/image/
 Insert Length: 2473 Std Err: 0.00
 Seq Primer: -40m13 fwd. Err from Amersham
 High quality sequence stop: 137.

FEATURES	SOURCE
Location/Qualifiers	
1. . 408	
/organism="Homo sapiens"	
/db_xref="Taxon:9606"	
/clone_id="NCL_CGAP_C03"	
/sex="pooled"	
/tissue_type="colon"	
/lab_host="DH10B"	
/note="Vector: pMT2D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. Library went through one round of normalization."	
BASE COUNT	107 a 76 c 61 g 164 t
Query Match	9.3%; Score 408; DB 2; Length 408;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2060 AGAAATCCGTCGGCATTAATGATGTTATGGTCAACTAAATTCAGAAATGCAA 2119
Db	408 AGAAATCCGTCGGCATTAATGATGTTATGGTCAACTAAATTCAGAAATGCAA 349
QY	2120 AAGGTCACATATCCCTGGAGCAGGAAACTTCACACATCATGGGAAATGGGTA 2179
Db	348 AAGGTCACATATCCCTGGAGCAGGAAACTTCACACATCATGGGAAATGGGTA 289
QY	2180 GCTCATCATGCTCGAAGAAATACAGAACTAGTAGAGAAGGGCTAGGGAGAATGGGTA 2239
Db	288 GCTCATCATGCTCGAAGAAATACAGAACTAGTAGAGAAGGGCTAGGGAGAATGGGTA 229
QY	2240 CAAATACATGCAAGAAGAGAGTCTCTGCTGATCTTTGATACATCCCTAT 2299
Db	228 CAAATACATGCAAGAAGAGAGTCTCTGCTGATCTTTGATACATCCCTAT 169
QY	2300 TAAAAAGGAGAGATACGGAGTTAAAGAGGCCATGGAAAACCTCTCTGTA 2359
Db	168 TTAAAAGGAGAGATACGGAGTTAAAGAGGCCATGGAAAACCTCTGTA 109
QY	2360 GCATCTACTCAGGCCAACAGGTATATGATATATAGCTGATAGAGCTGTTAGTT 2419
Db	108 GCATCTACTCAGGCCAACAGGTATATGATATATAGCTGATAGAGCTGTTAGTT 49
QY	2420 ACATGTTATGGCTTAATTATTAATTAATCACAACATCTG 2467
Db	48 ACATGTTATGGCTTAATTATTAATTAATCACAACATCTG 1